

Fig. 1

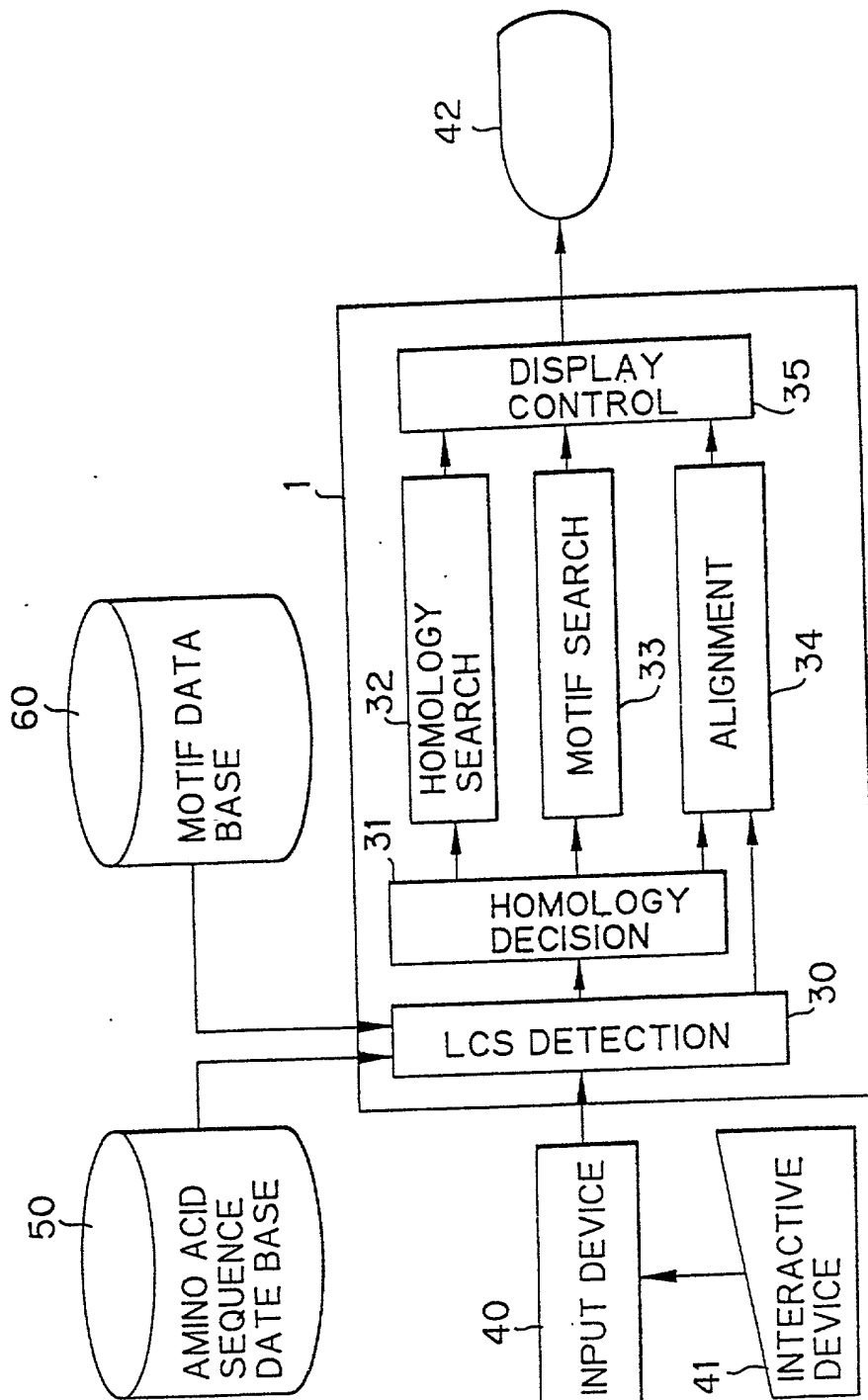


Fig. 2

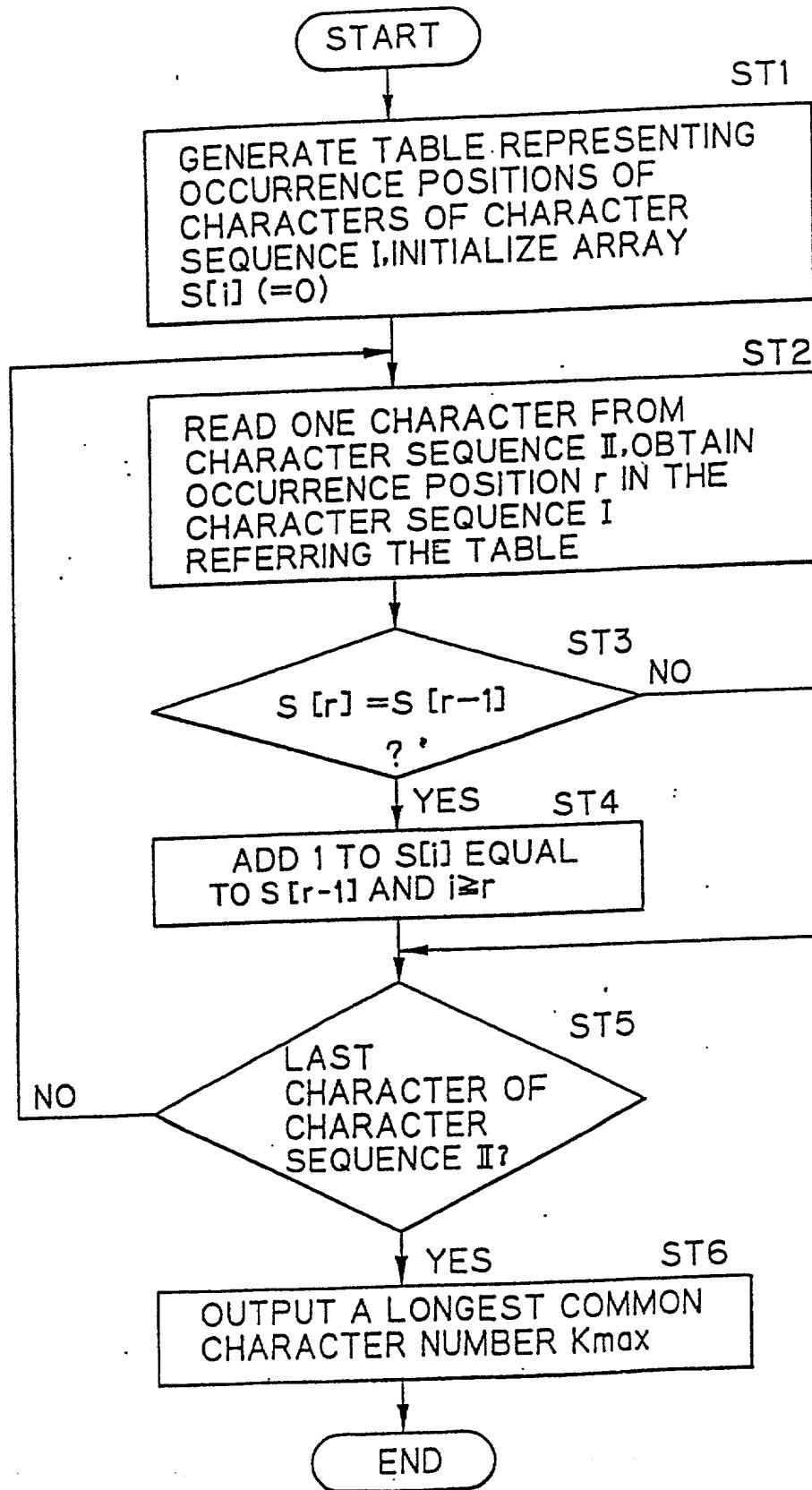


Fig. 3

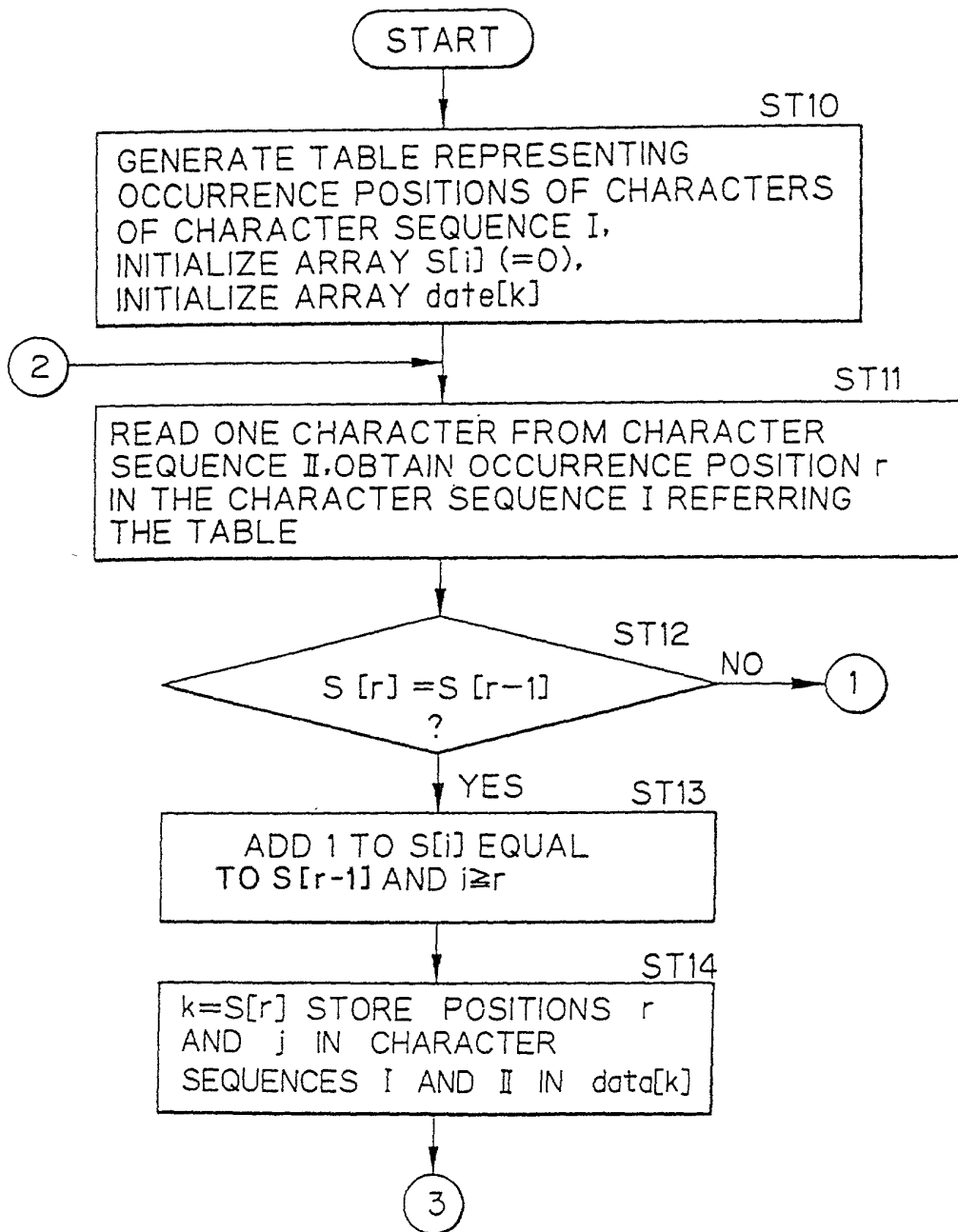


Fig. 4

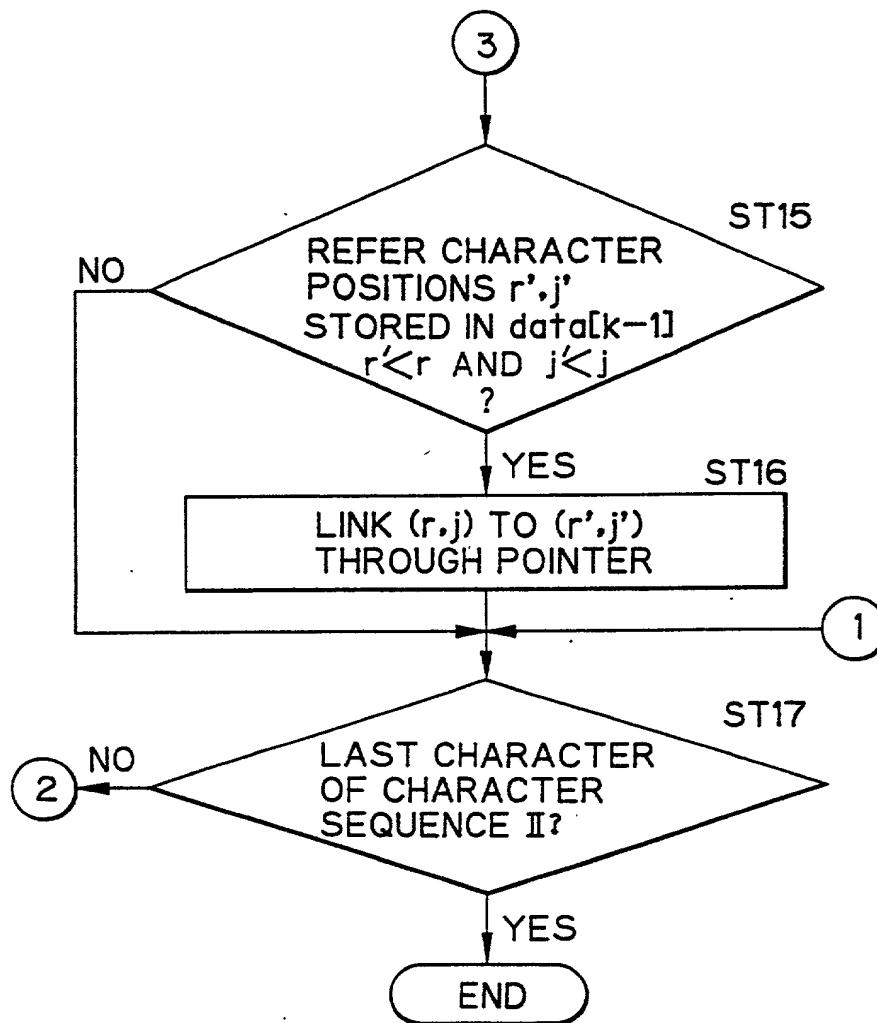


Fig. 5

CHARACTER SEQUENCE I="ABCB DAB"

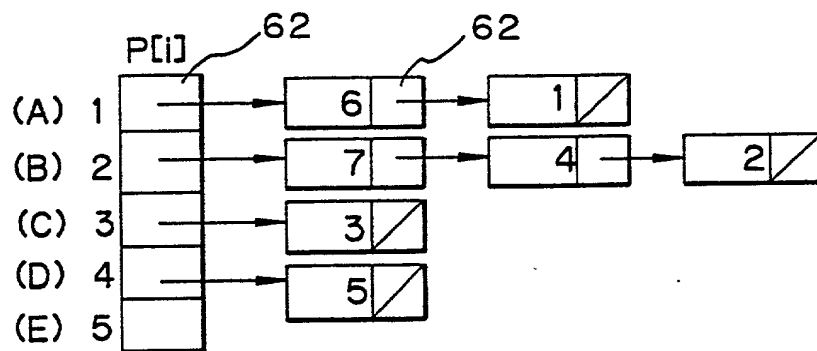


Fig. 6

CHARACTER SEQUENCE II = "BDCABA"

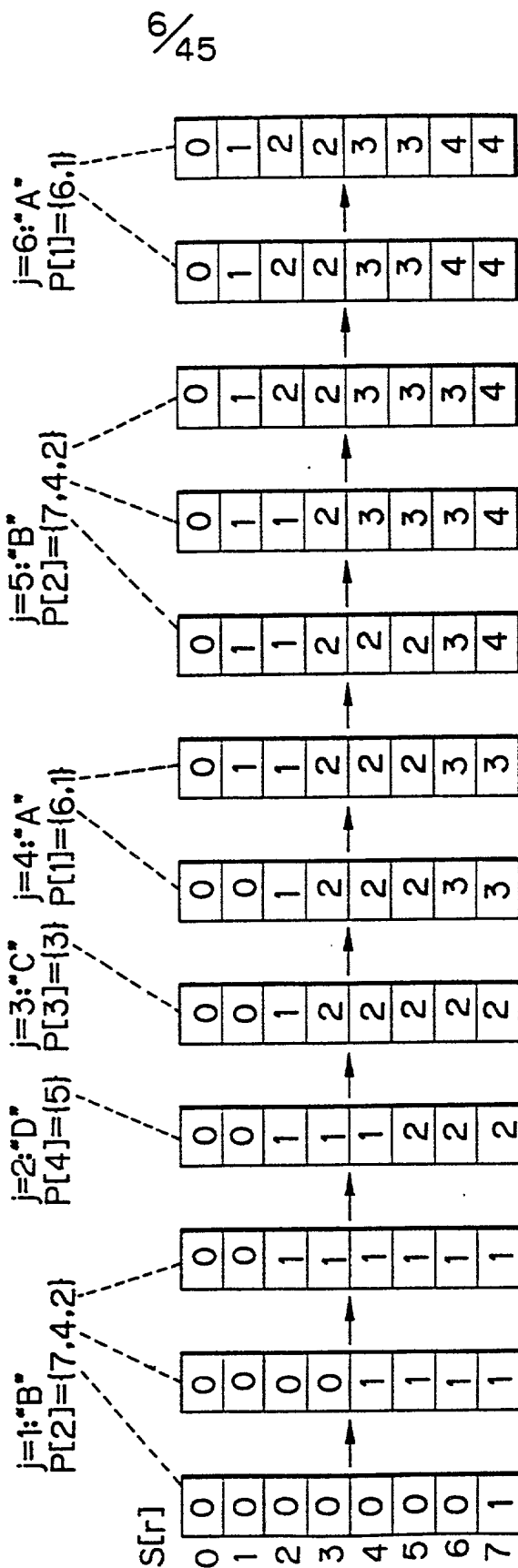


Fig. 7

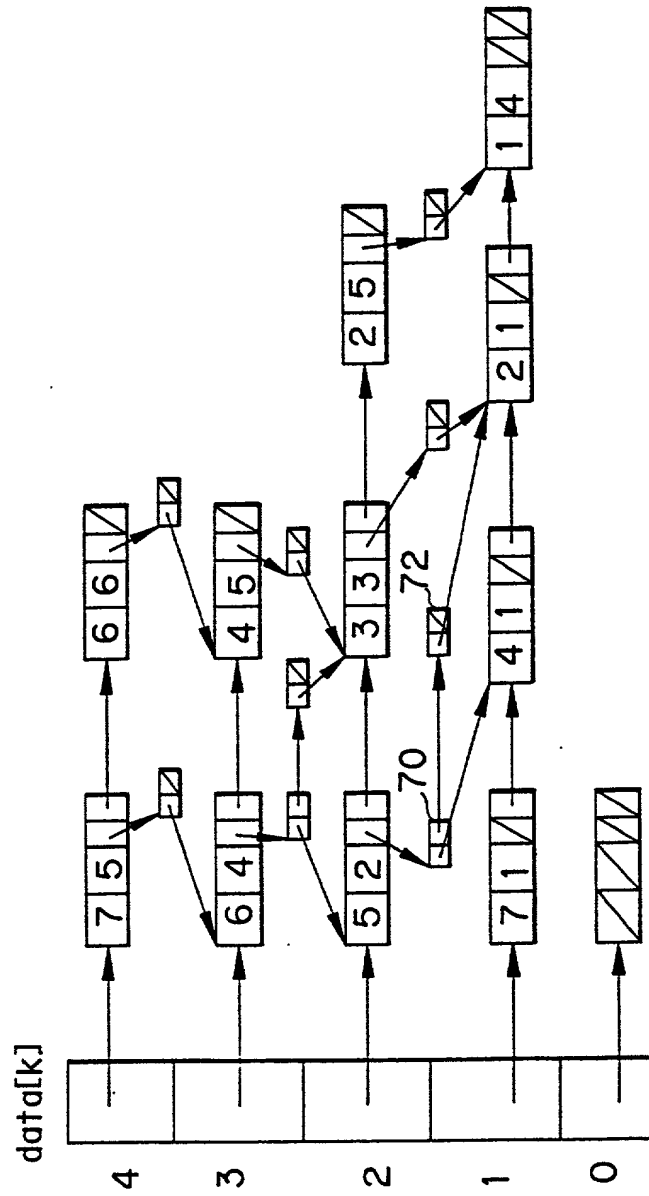


Fig. 8

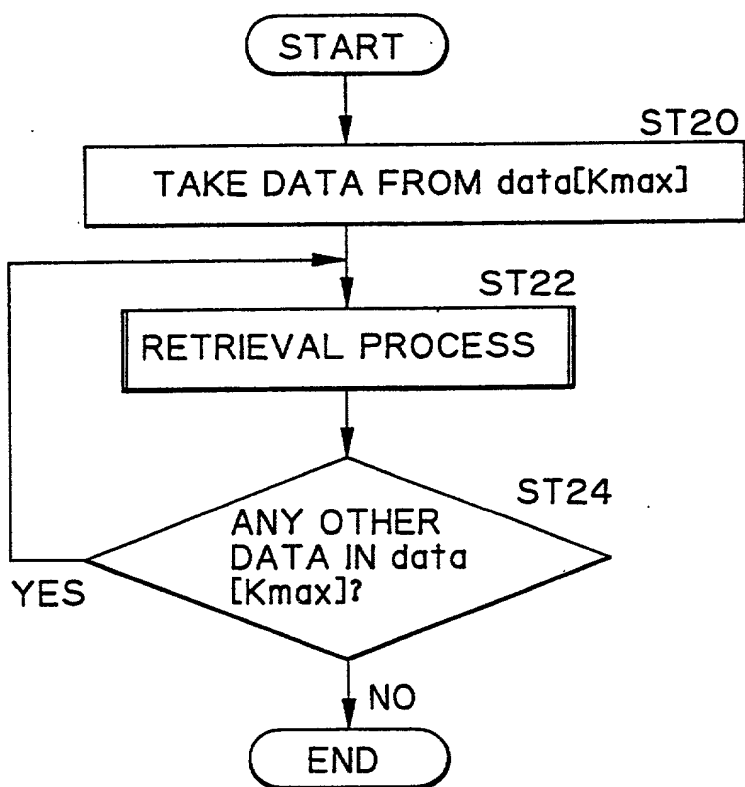


Fig. 9

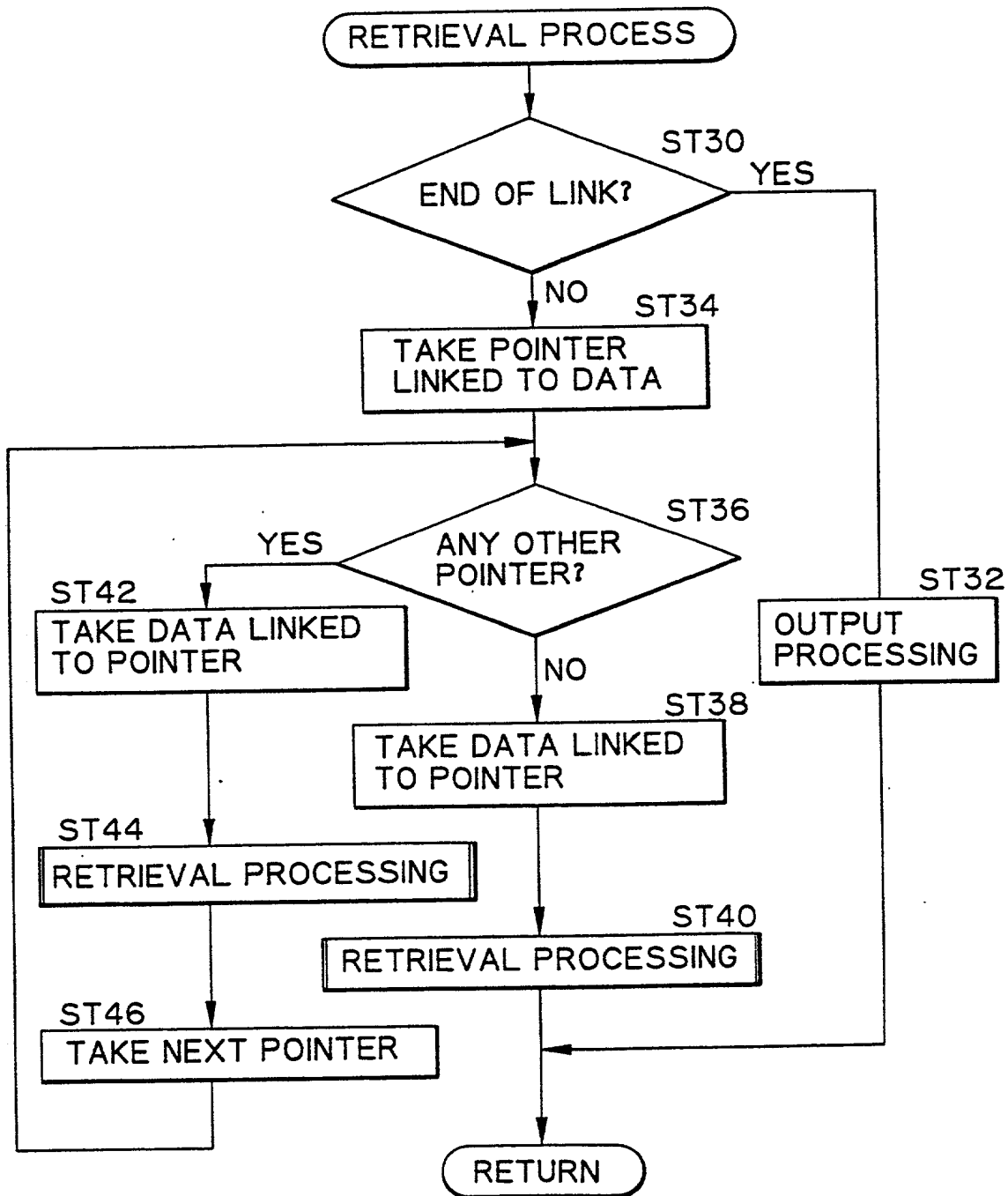


Fig. 10

human : GDVEKGKKIFIMKCSQCHTVEGGKHKTGPNLHGLFGRK
bacterium : EGDAAAGEKVSCKLACHTFDQGGANKVGPNNLFGVF

LCS : GD{x3.3}G{x0.1}K{x0.2}K{x4.0}KC{x2.2}CHT{x3.3}GG{x2.2}K
GD{x1.4}E{x0.2}K{x0.2}K{x0.4}KC{x2.2}CHT{x3.3}GG{x2.2}K

homology : 47%

Fig. 11

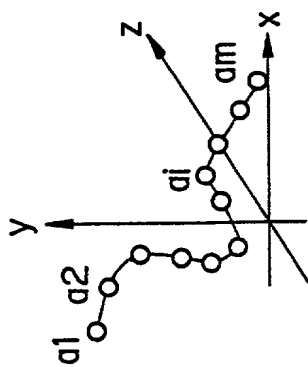
Rat : MSLAILRVIRLVRVFRIFKLSRHSGKLQILGRTLKASMRGLGLIFFIGVV

leucinzip. L(6)L(6)L(6)L(6)L

Fig. 12

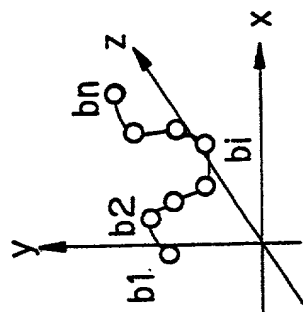
human : GDVEK G K KIFIMKCSQCHTVEKGG KHKTGPNLHGLFGRK ...
bacterium : E GDAAAGEKVS KCLACHTFDQGGANKV GPNPN LFGVF...

Fig. 13 A



$$A = \{a_1, a_2, \dots, a_i, \dots, a_m\}$$

Fig. 13 B



$$B = \{b_1, b_2, \dots, b_j, \dots, b_n\}$$

Fig. 13 C

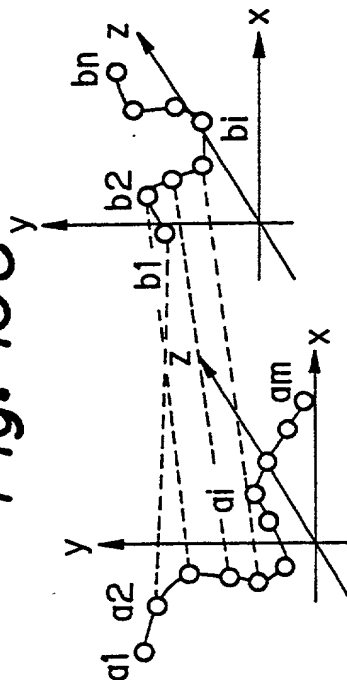


Fig. 13 D

$$r.m.s.d = \frac{\sqrt{\sum_{k=1}^n w_k (U_{b_k} - a_k)^2}}{n}$$



Fig. 15

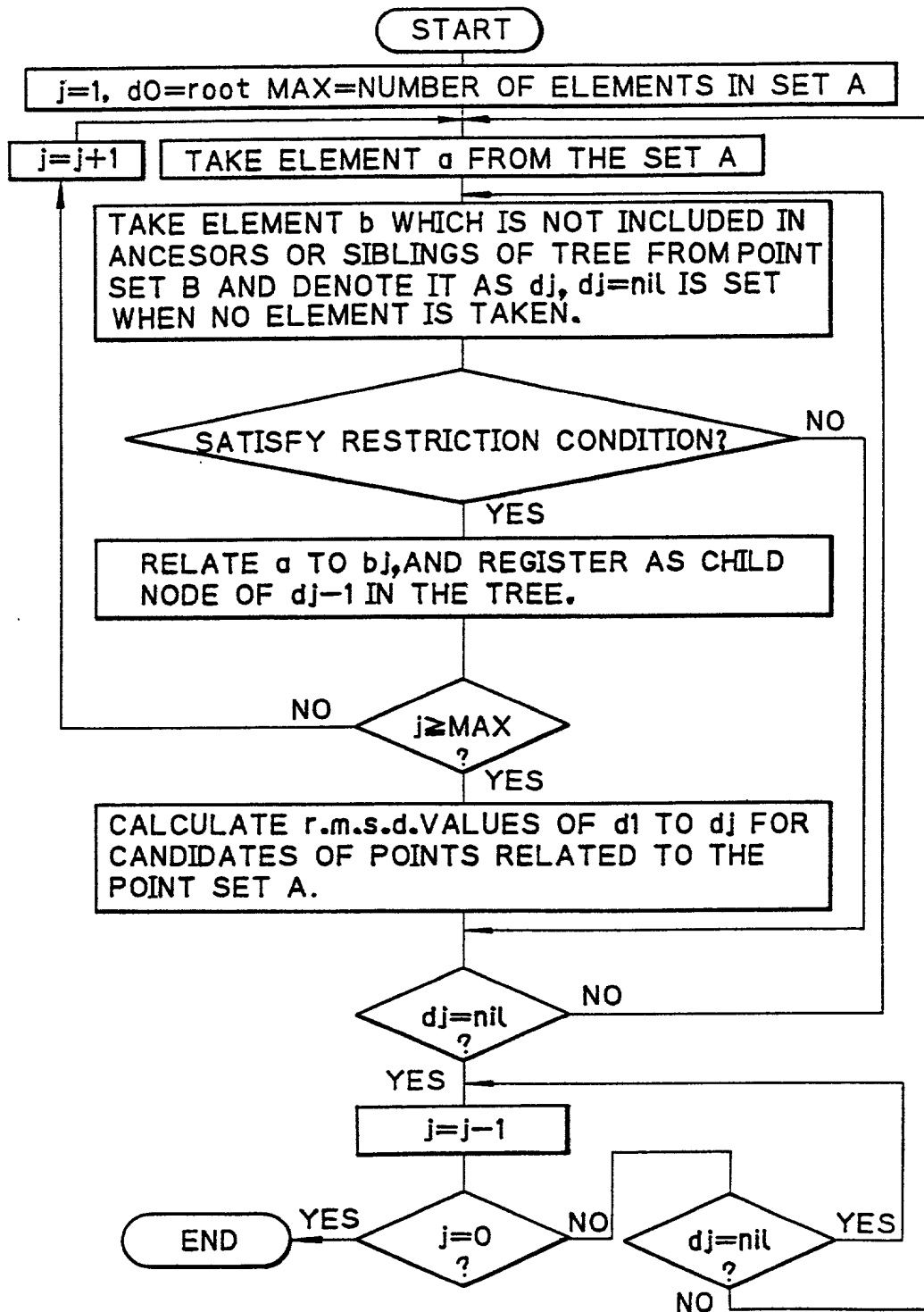


Fig. 14 A

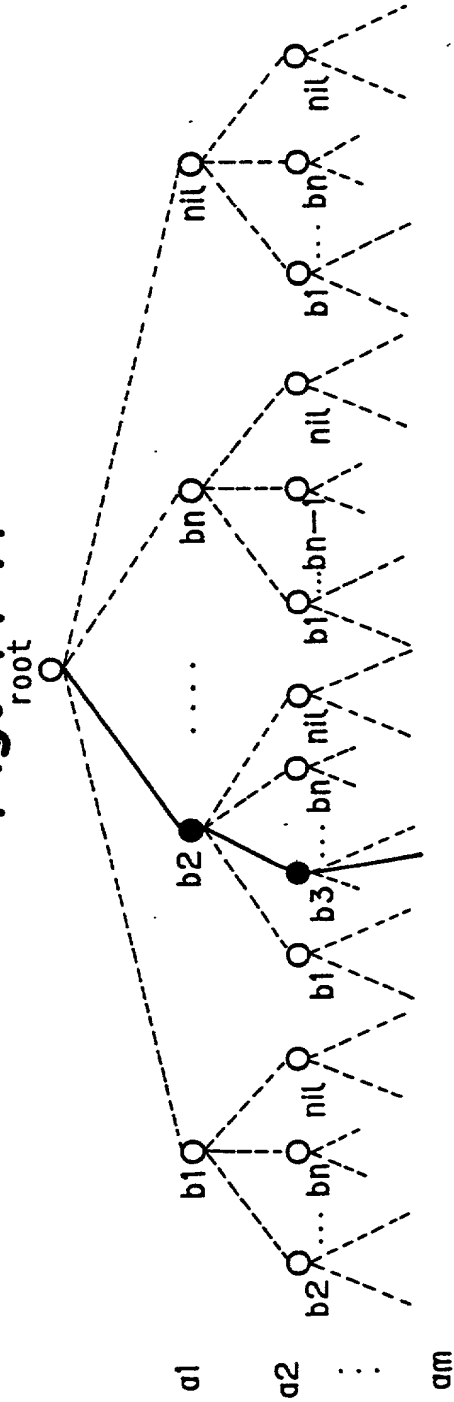


Fig. 14 B

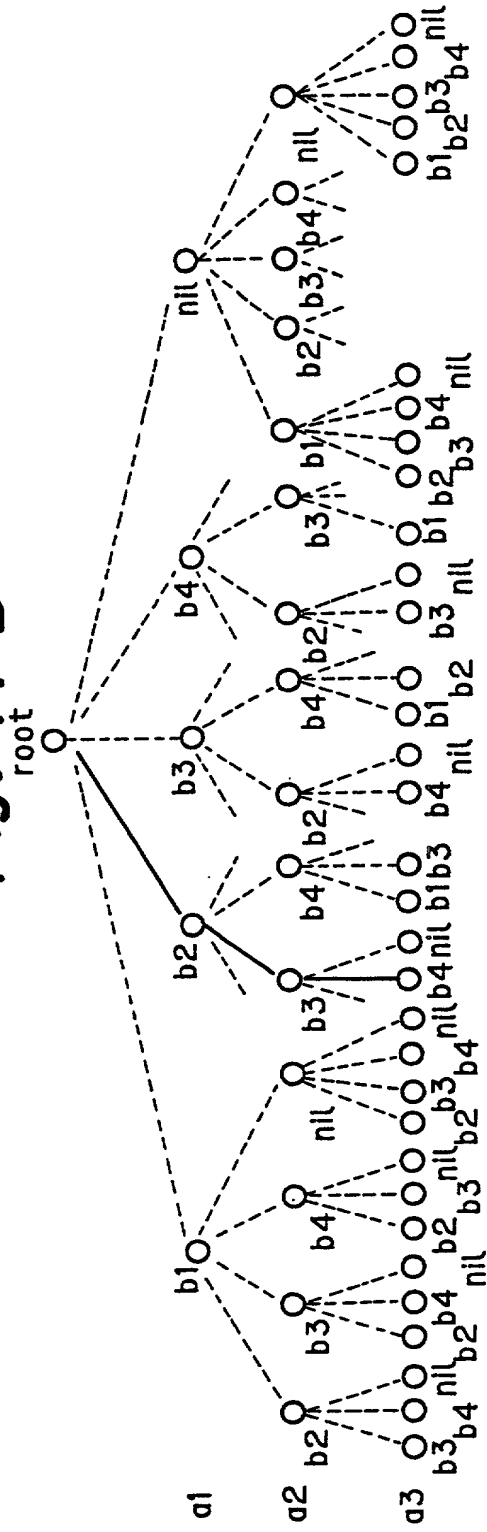


Fig. 16 A

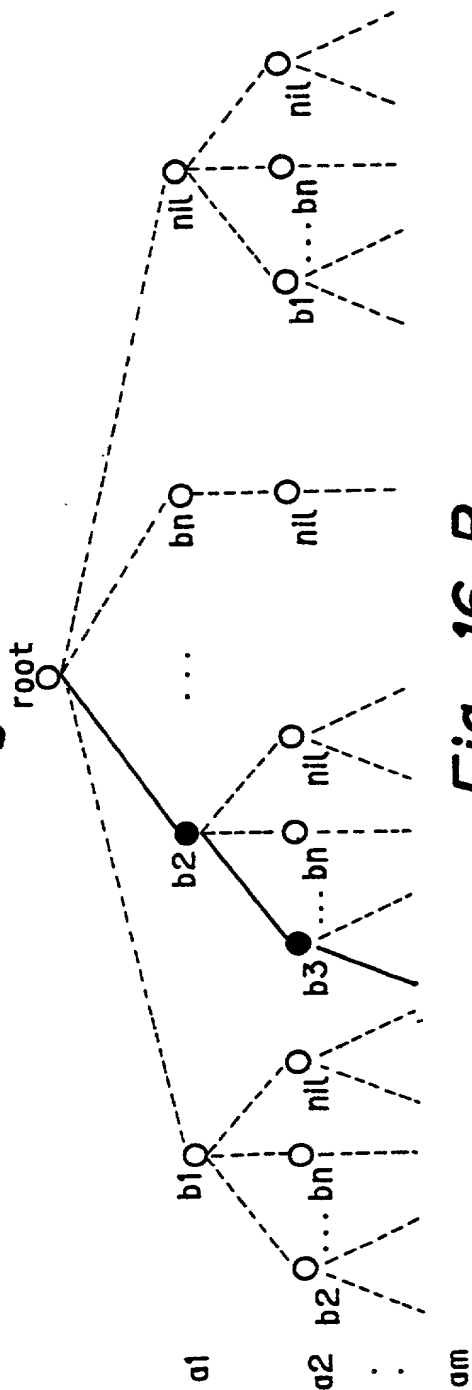


Fig. 16 B

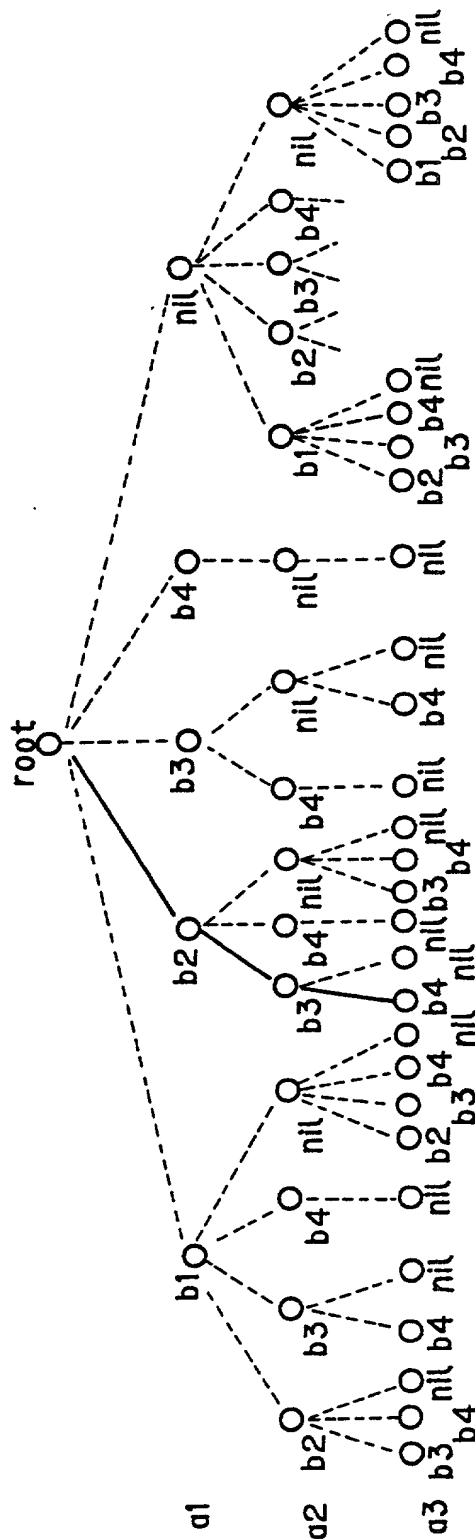


Fig. 17

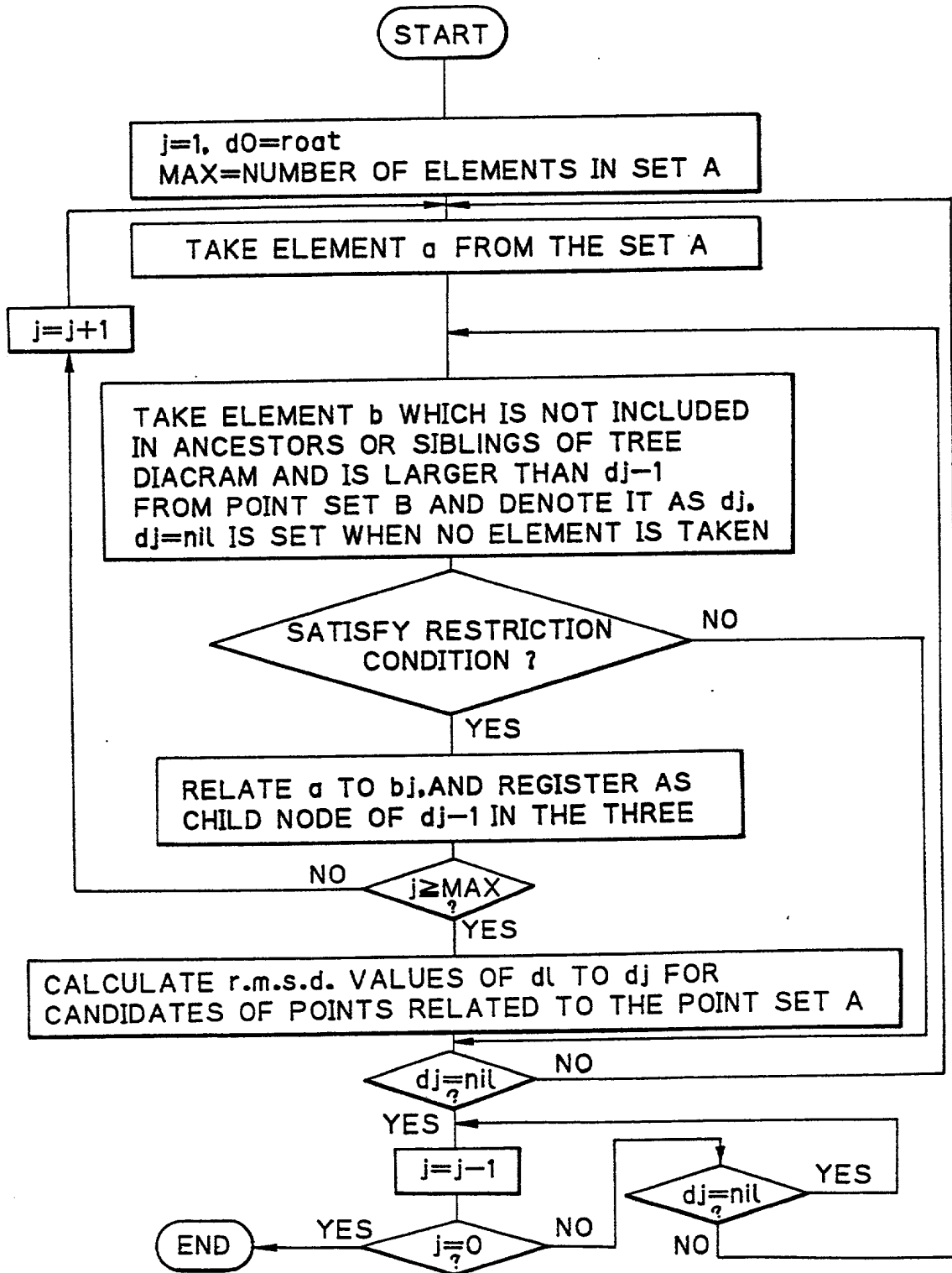


Fig. 18

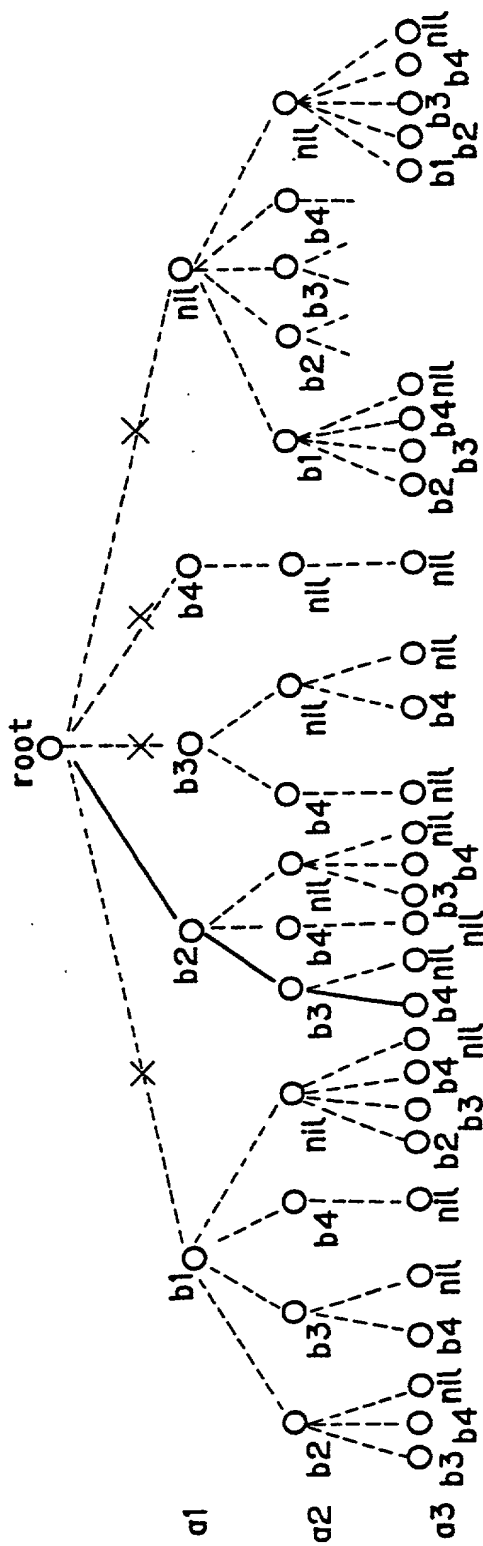


Fig. 19 A

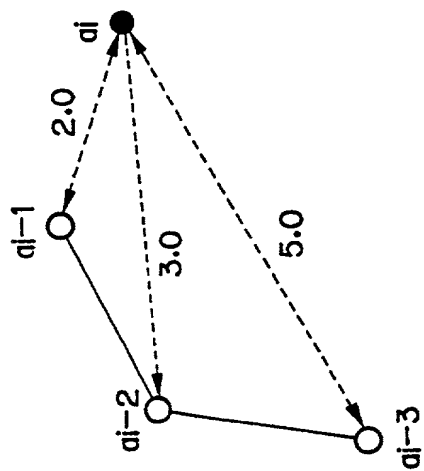


Fig. 19 B

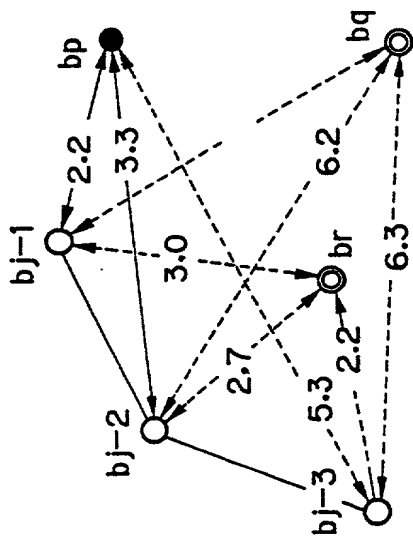


Fig. 20 A

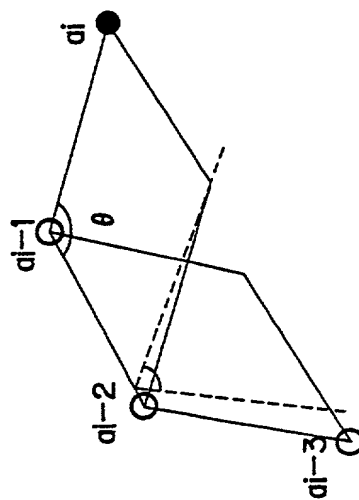


Fig. 20 B

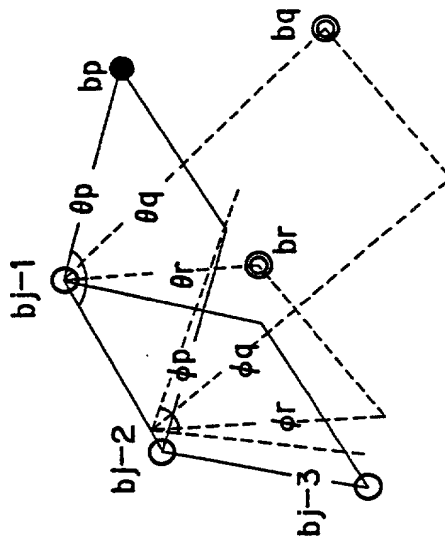


Fig. 21

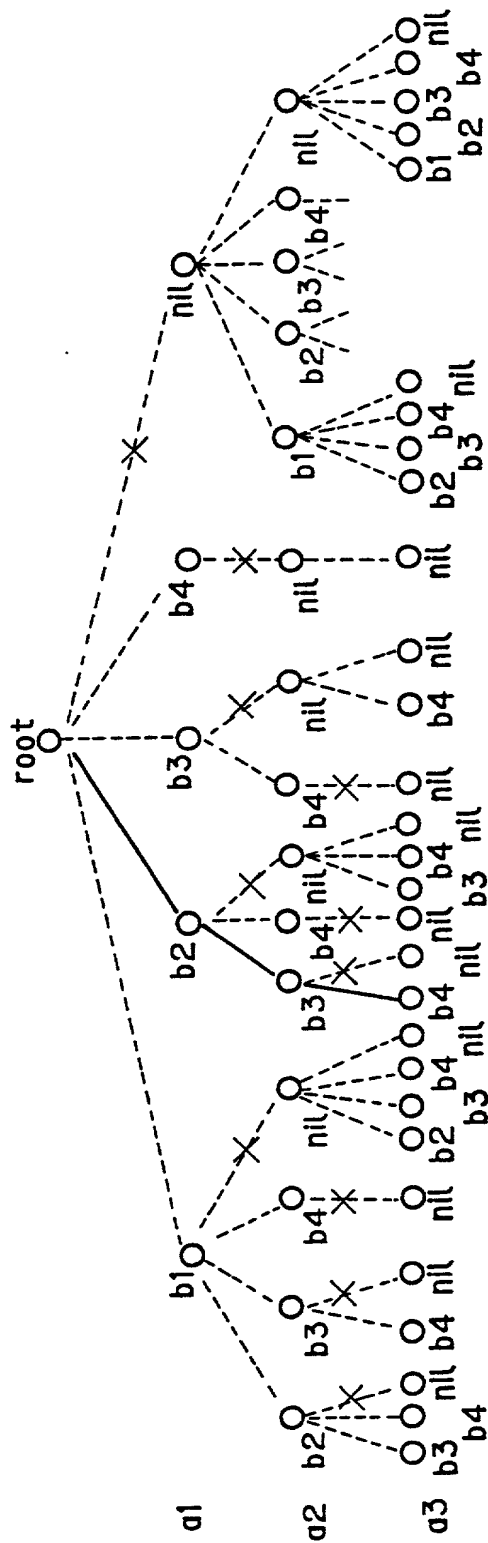


Fig. 22

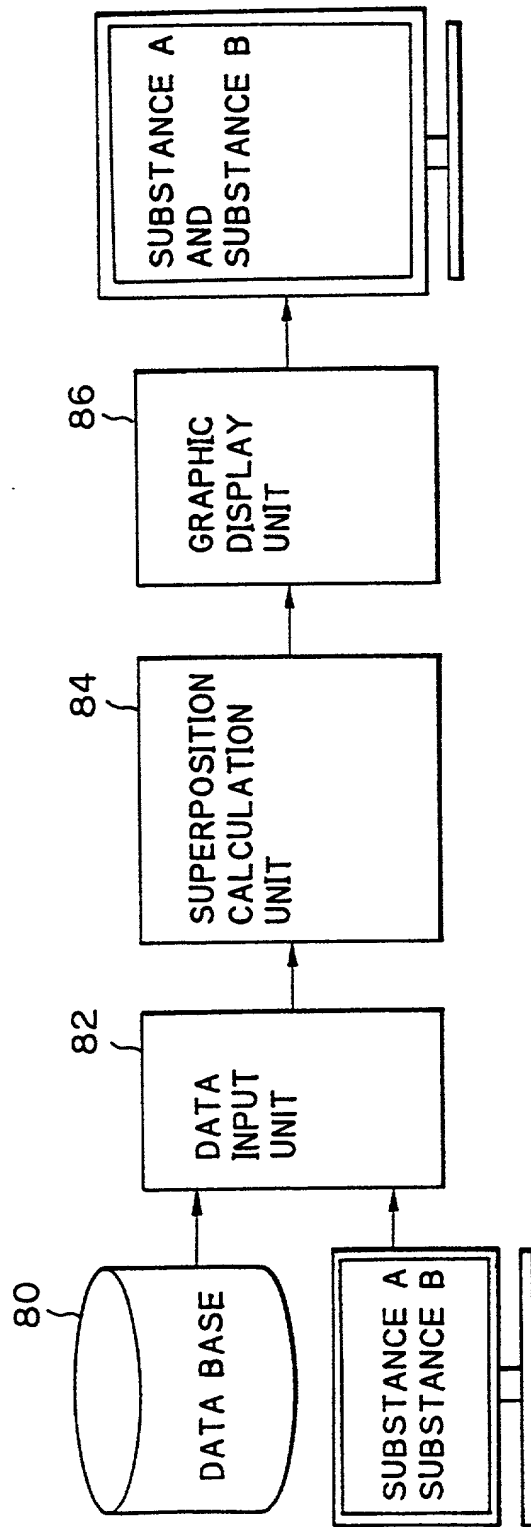


Fig. 23 A

1	TEEQIAEFKE	AFSLFDKDG
21	GTITTKELGT	VMRSLGQNPT
41	EAELQDMINE	VDADGNGTID
61	FPEFLTMMAR	KMKD TDSEEE
81	IREAFRVFDK	DGNGYISAAE
101	LRHVMTNLGE	KLTD EEVDEM
121	IREANIDGDG	QVNYEEFVQM
141	MTA	

AMINO ACID SEQUENCE OF CALMODULIN
(EXCERPT FROM PDB)

Fig. 23 B

1	AMDQQAEARA	FLSEEMIAEF
21	KAAFD MF DAD	GGGDI STKEL
41	GTVMRMLGQN	PTKEELDAII
61	EEVDE DGS GT	IDFEEFLVM
81	VRQMKEDAKG	KSEEEELADCF
101	RIFDKNADGF	IDIEELGEIL
121	RATGEHVTEE	DIEDLMKDSD
141	KNNDGRIDFD	EFLKMMEGVQ
161		

AMINO ACID SEQUENCE OF TROPONIN C
(EXCERPT FROM PDB)

Fig. 24 A

CALMODULIN

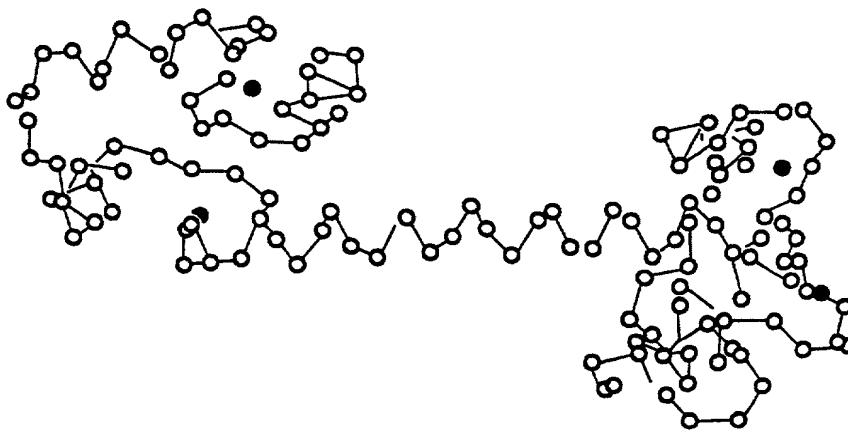


Fig. 24 B

TROPONIN C

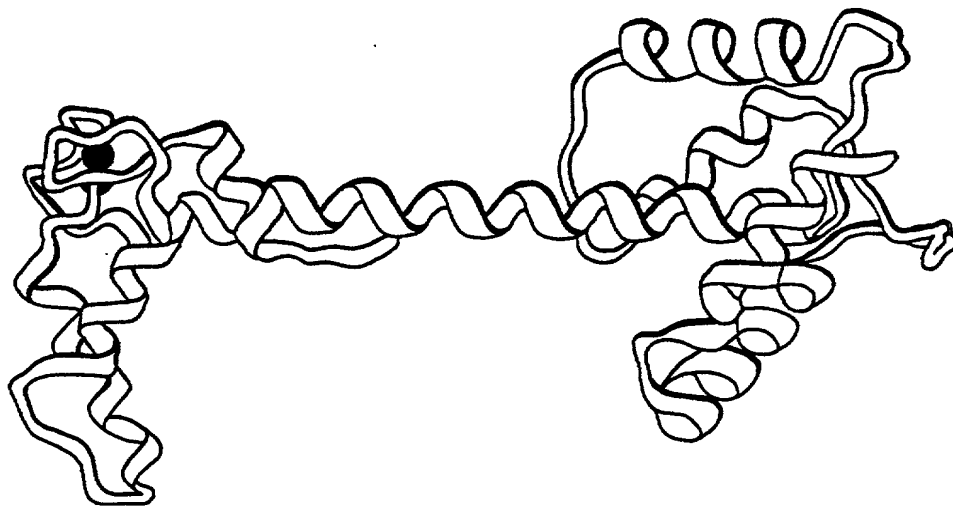


Fig. 26

96	L	A	D	C	F	R	I	F	D	K	N	A	D	G	F	< target	>
97	I	R	E	A	F	R	V	F	D	K	D	G	N	G	Y	< probe	>
98	I	D	I	E	E	E	L	G	E	I	L	R	A	T	< target	>	
99	I	S	A	A	E	E	L	R	H	V	M	T	N	L	< probe	>	
100	I	E	D	I	L	M	K	D	S	D	K	N	N	D	G	< target	>
101	V	D	E	M	I	R	E	A	A	N	I	D	G	D	G	< probe	>
102	R	I	D	F	D	E	F	L	K	M	M	M	E	G	< target	>	
103	Q	V	N	Y	E	E	F	V	V	Q	M	M	T	A	< probe	>	

rmsd = 0.823665

Fig. 27

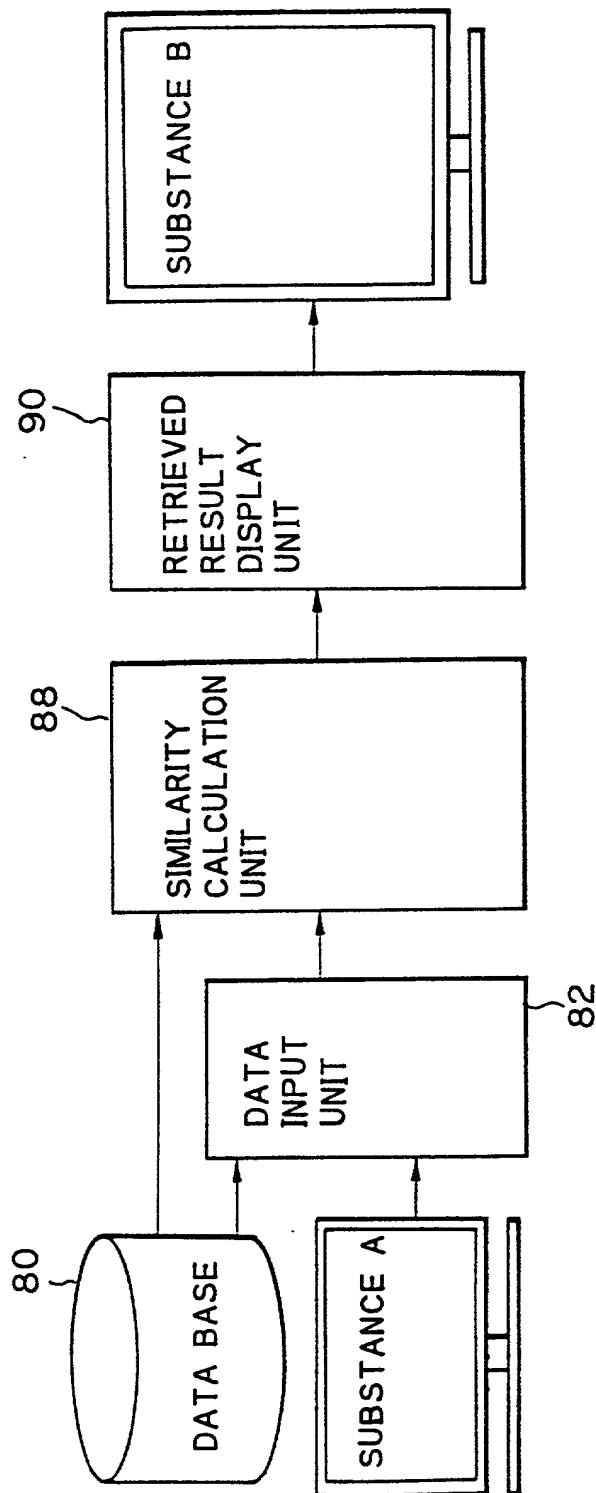
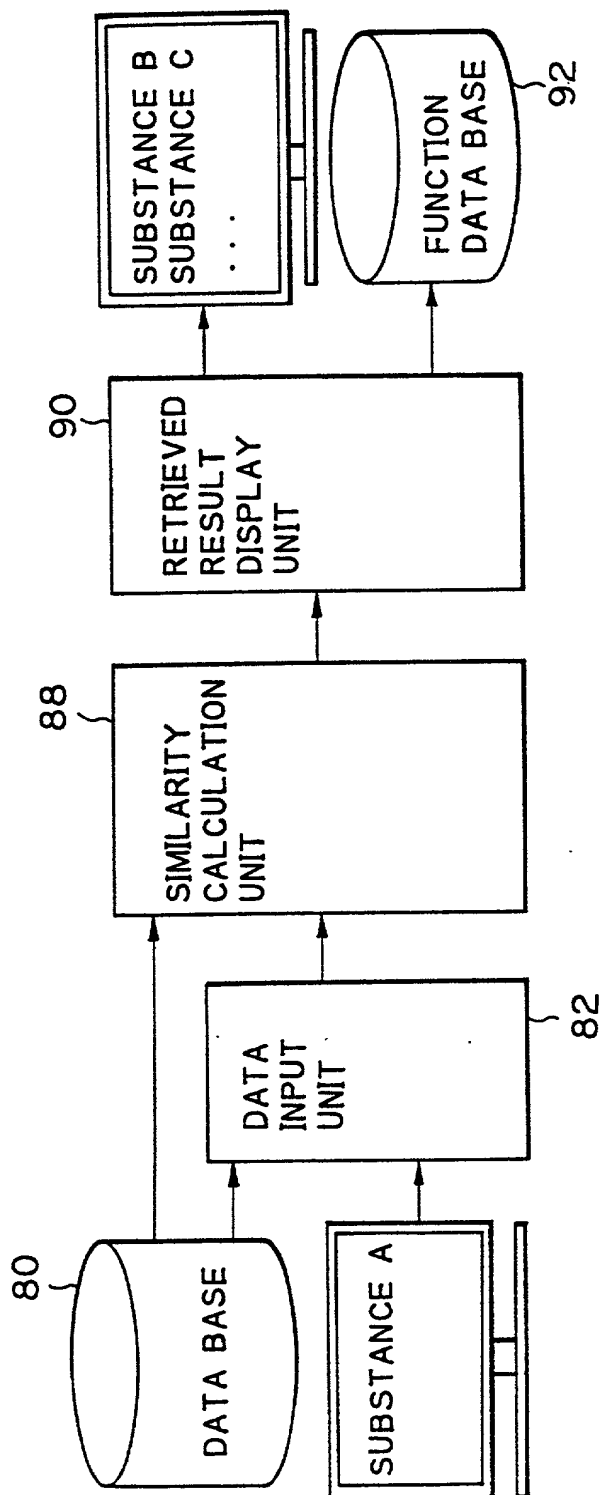


Fig. 28



FOE220"60860660

Fig. 29

===== ATP/GTP binding site =====

Probe = (elongation factor)

7 8 9 10 11 12 13 14
G H V D H G K T < probe >

8 9 10 11 12 13 14 15
G A P G S G K G < target >
G H V D H G K T < probe >
rmsd=0.648732 adenylate kinase

unit - A

. : . : .
10 11 12 13 14 15 16 17
G A G G V G K S < target >
G H V D H G K T < probe >
rmsd=0.421770 ras protein

Fig. 30

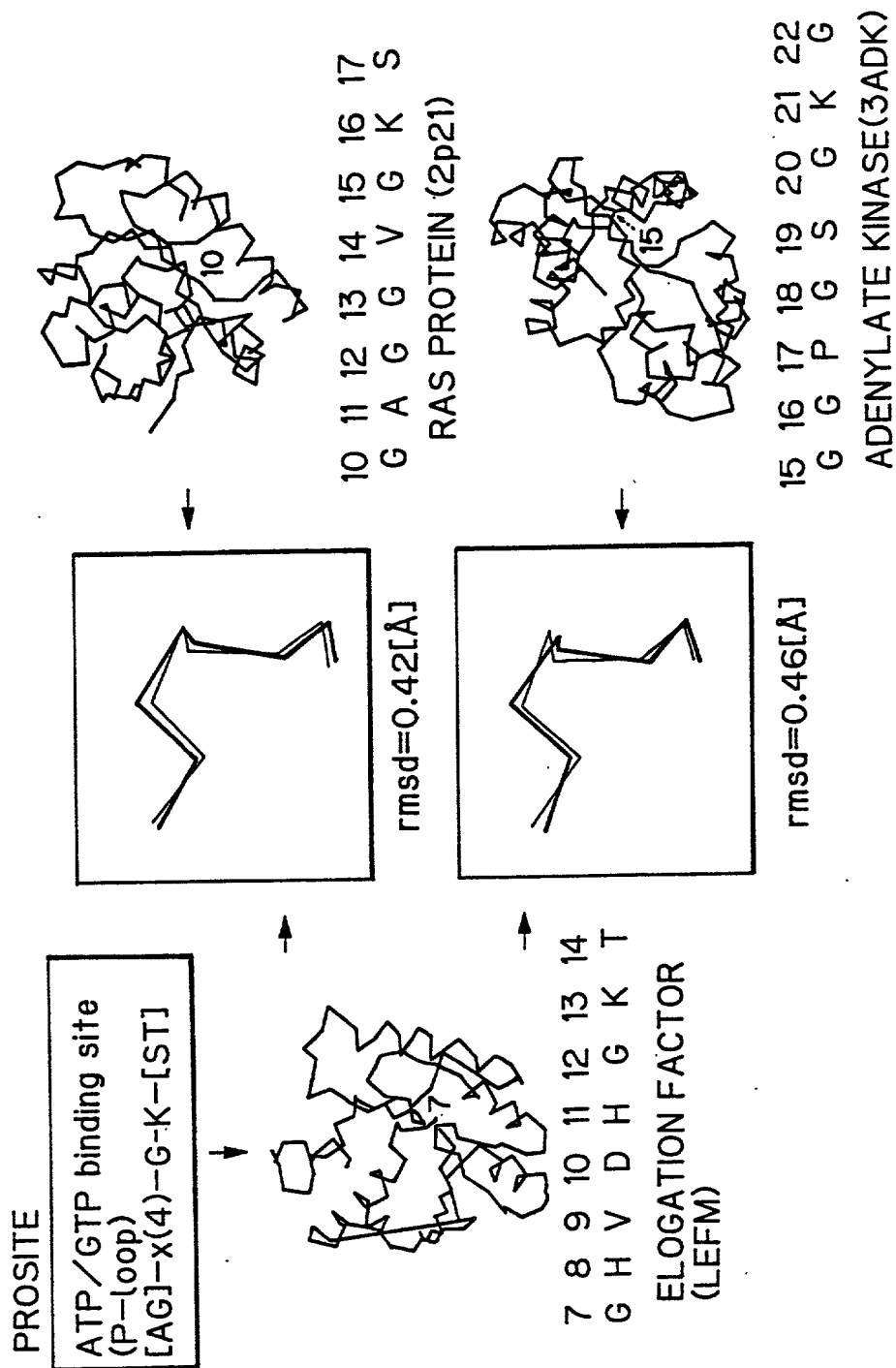


Fig. 31

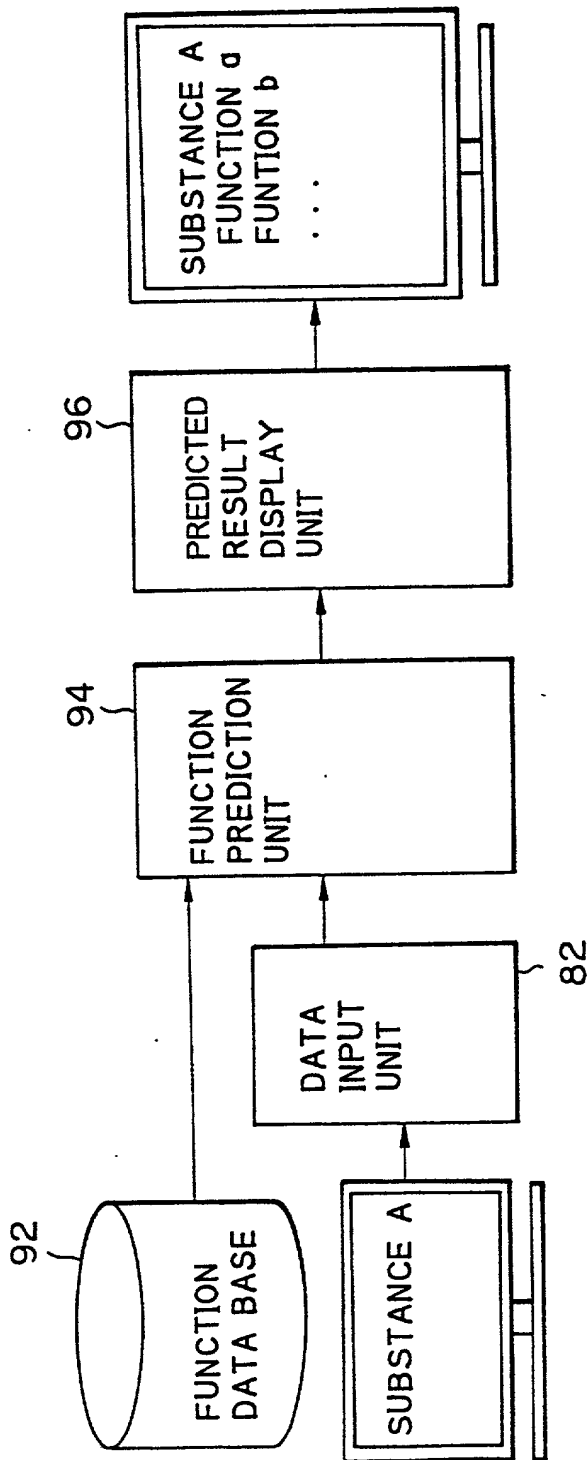


Fig. 32 A

Fig. 32 B

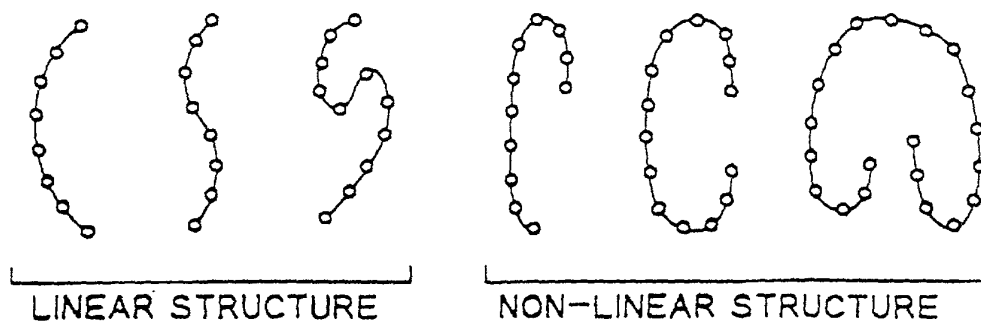
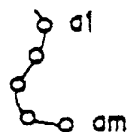
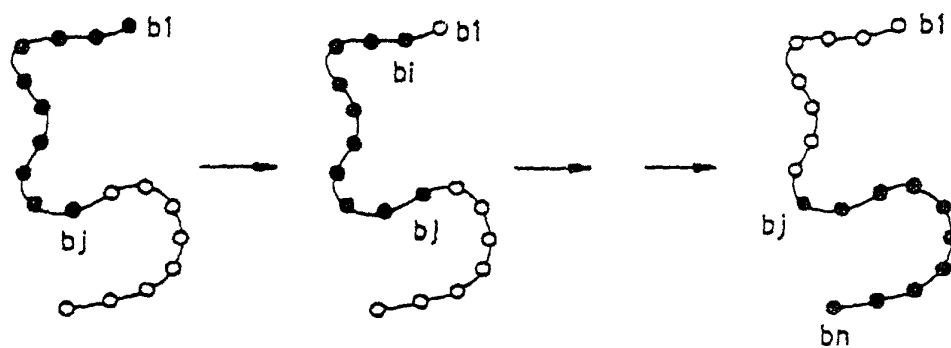


Fig. 33

WHEN $f(x)=2x$



$A=\{a_1, \dots, a_m\}$



$B=\{b_1, \dots, b_i, \dots, b_j, \dots, b_n\}$

FOU220 60860660

Fig. 34

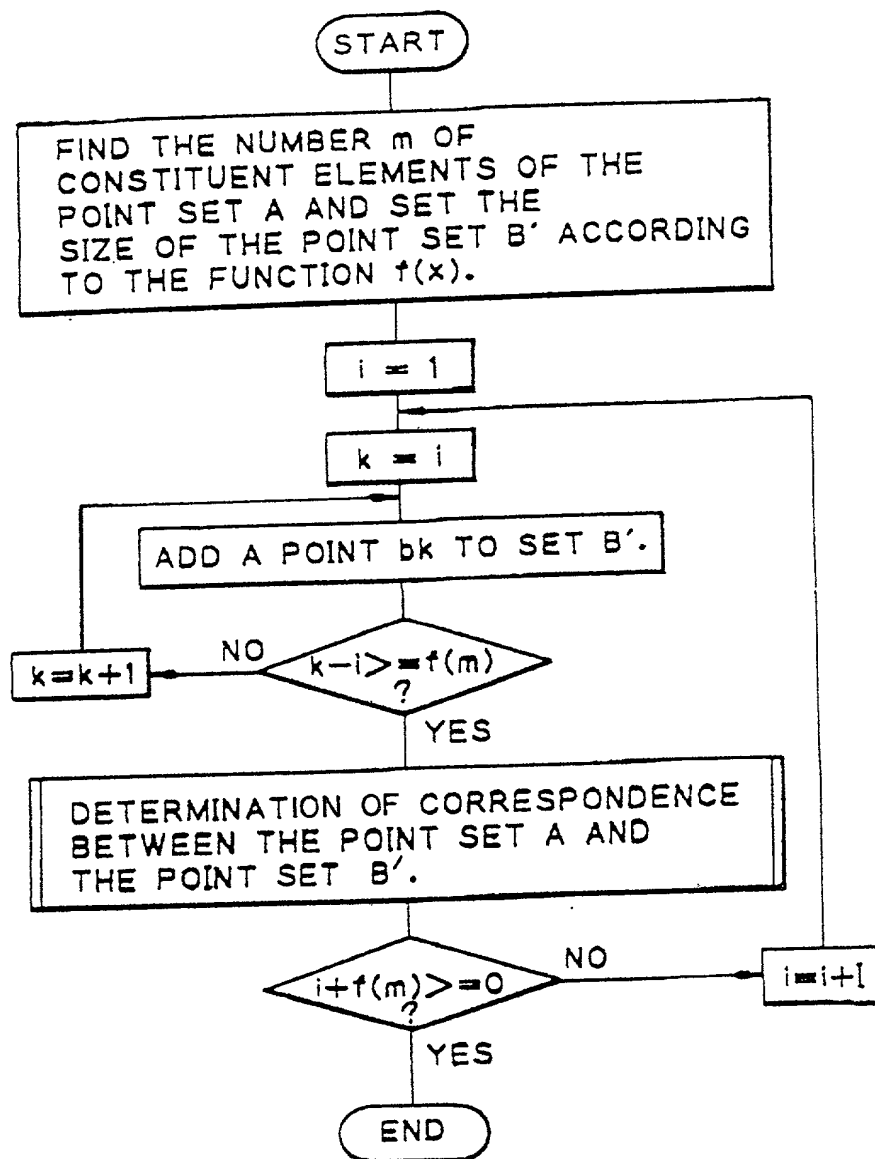
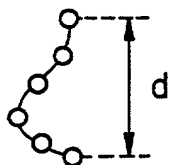
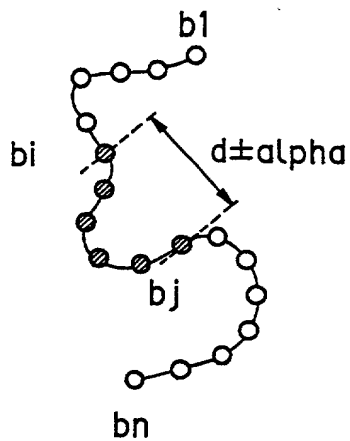


Fig. 35 A



$$A = \{a_1, a_2, \dots, a_m\}$$

Fig. 35 B



$$B = \{b_1, \dots, b_i, \dots, b_j, \dots, b_n\}$$

Fig. 36

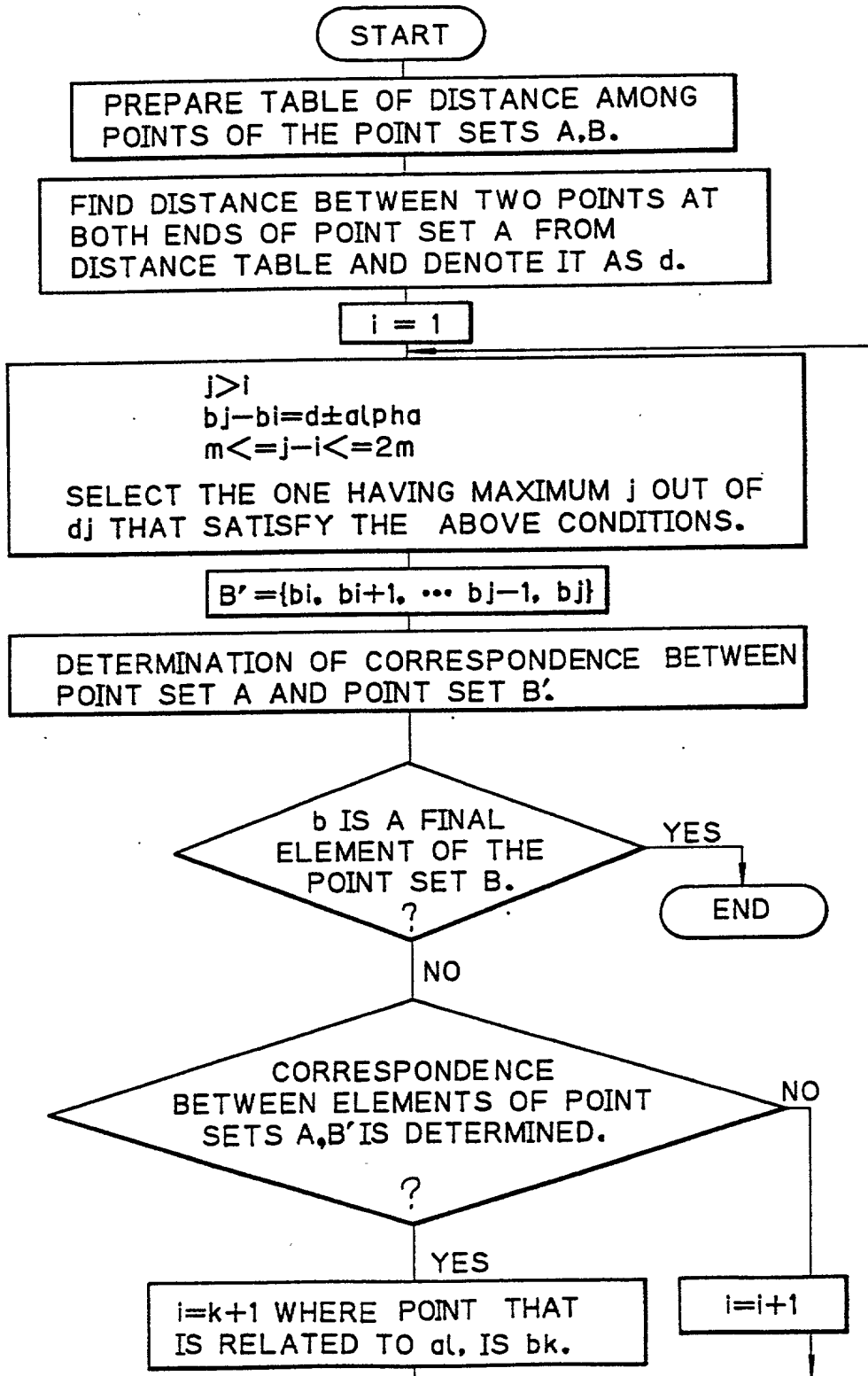
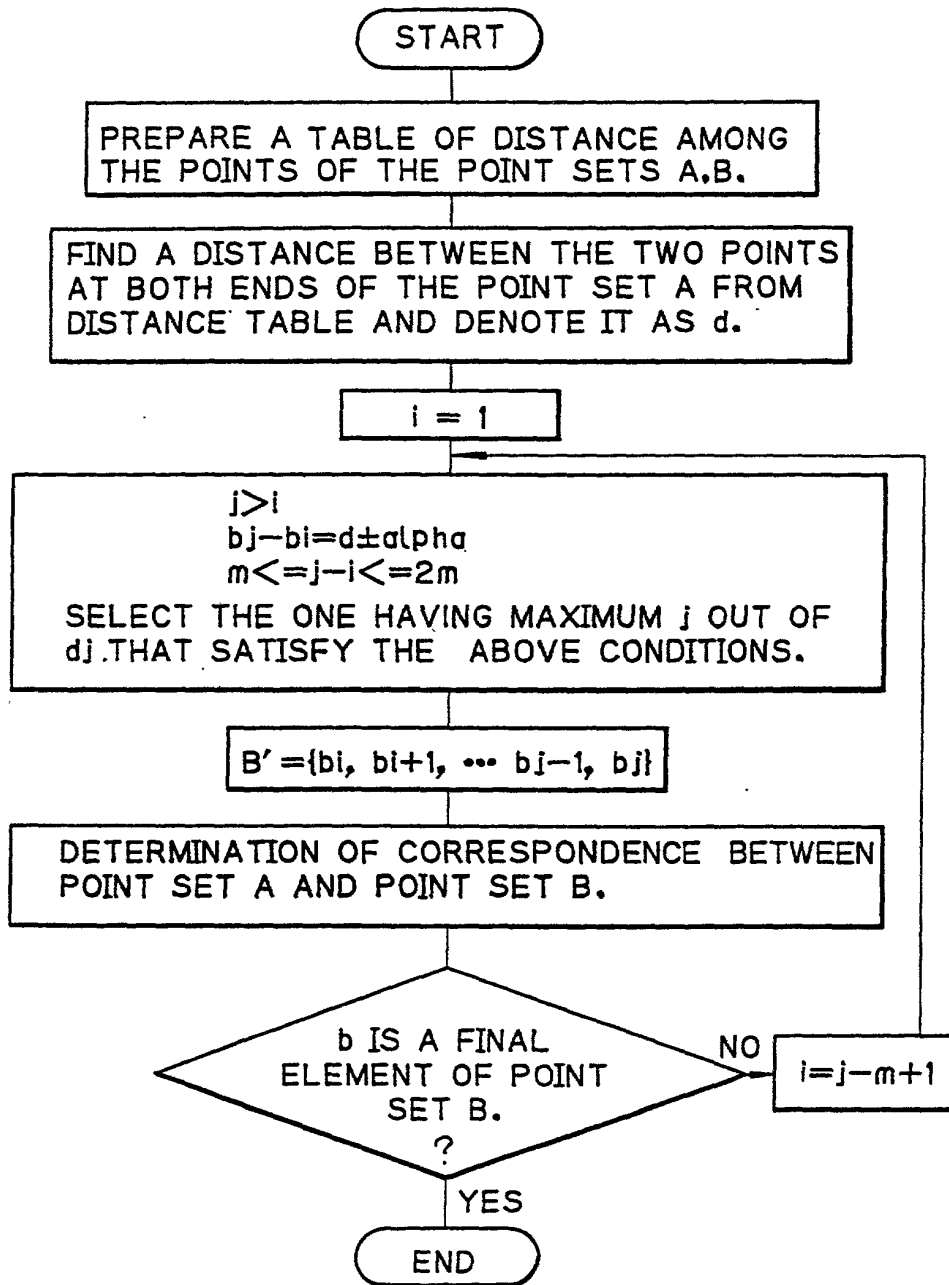


Fig. 37



T0220 60860660

Fig. 38 A

1	I	V	G	G	Y	T	C	C	A	N	T	V	P	Y	Q	V	S	L	N	S
21	G	Y	H	F	C	G	G	S	L	I	N	S	Q	W	V	V	S	A	A	H
41	C	Y	K	S	G	I	Q	V	R	L	G	E	D	N	I	N	V	V	E	G
61	N	E	Q	F	I	S	A	S	K	S	I	V	H	P	S	Y	N	S	N	T
81	L	N	N	D	I	M	L	I	K	L	K	S	A	A	S	L	N	S	R	V
101	A	S	I	S	L	P	T	S	C	A	S	A	G	T	Q	C	L	I	S	G
121	W	G	N	T	K	S	S	G	T	S	Y	P	D	V	L	K	C	L	K	A
141	P	I	L	S	D	S	S	C	K	S	A	Y	P	G	Q	I	T	S	N	M
161	F	C	A	G	Y	L	E	G	G	K	D	S	C	Q	G	D	S	G	G	P
181	V	V	C	S	G	K	L	Q	G	I	V	S	W	G	S	G	C	A	Q	K
201	N	K	P	G	V	Y	T	K	V	C	N	Y	V	S	W	I	K	Q	T	I
221	A	S	N																	

AMINO ACID SEQUENCE OF TRYPSIN (EXCERPT FROM PDB)

Fig. 38 B

1	V	V	G	G	T	E	A	Q	R	N	S	W	P	S	Q	I	S	L	Q	Y
21	R	S	G	S	S	W	A	H	T	C	G	G	T	L	I	R	Q	N	W	V
41	M	T	A	A	H	C	V	D	R	E	L	T	F	R	V	V	V	G	E	H
61	N	L	N	Q	N	N	G	T	E	Q	Y	V	G	V	Q	K	I	V	V	
81	P	Y	W	N	T	D	D	V	A	A	G	Y	D	I	A	L	L	R	L	A
101	Q	S	V	T	L	N	S	Y	V	Q	L	G	V	L	P	R	A	G	T	I
121	L	A	N	S	P	C	Y	I	T	T	G	W	G	L	T	R	T	N	G	Q
141	L	A	Q	T	L	Q	Q	A	Y	L	P	T	V	D	Y	A	I	C	S	S
161	S	S	Y	W	G	S	T	V	K	N	S	M	V	C	A	G	G	D	G	V
181	R	S	G	C	Q	G	D	S	G	G	P	L	H	C	L	V	N	G	Q	Y
201	A	V	H	G	V	T	S	F	V	S	R	L	G	C	N	V	T	R	K	P
221	T	V	F	T	R	V	S	A	Y	I	S	W	I	N	N	V	I	A	S	N

AMINO ACID SEQUENCE OF ELASTASE (EXCERPT FROM PDB)

Fig. 39 A

Key site number 36 - 41 in Trypsin

41 42 43 44 45 46

41 42 43 44 45 46 < target >
M T A A H C

V S A A H C < probe >

$$d = 12.070038 \text{ [Å]}$$
$$\text{r.m.s.d.} = 0.061077 \text{ [Å]}$$

The number of atoms in a probe = 6

The number of atoms in PDB = 240

The number of combination = 1

Time = 1sec

RETRIEVED RESULTS OF HISTIDINE ACTIVE SITES

Fig. 39 B

Key site number 175 - 179 in Trypsin

186 187 188 189 190

G D S G G < target >

G D S G G < probe >

$$d = 8.922721 \text{ [A]}$$

```
r.m.s.d. = 0.092879 [A]
```

The number of atoms in a probe = 5

The number of atoms in PDB = 240

The number of combination = 1

Time = 1sec

RETRIEVED RESULTS OF SERINE ACTIVE SITES

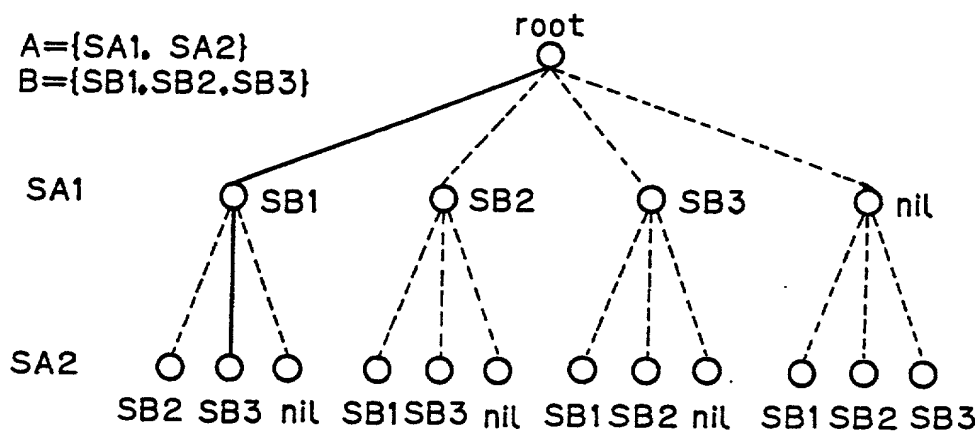
Fig. 40

Fig. 41

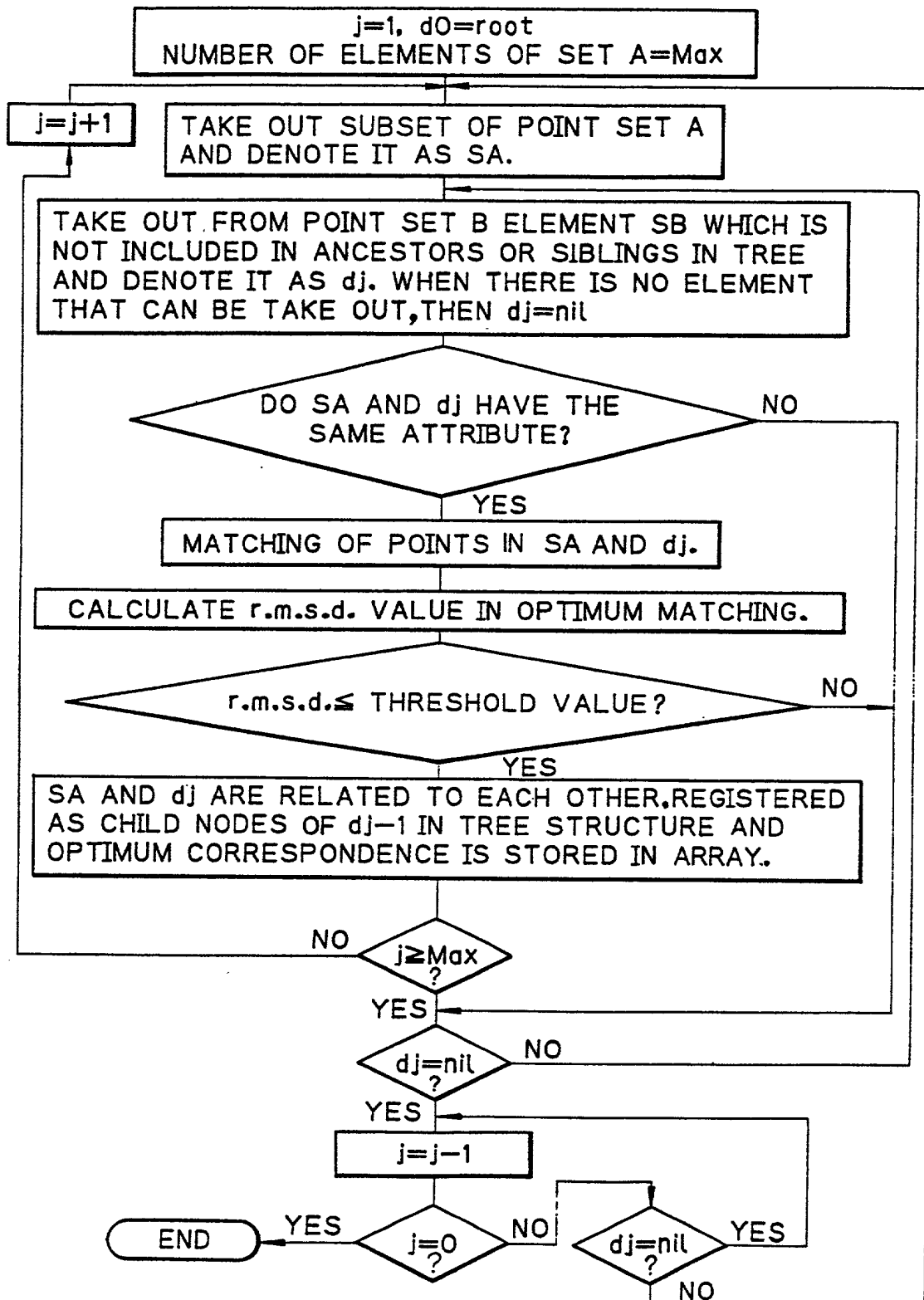


Fig. 42

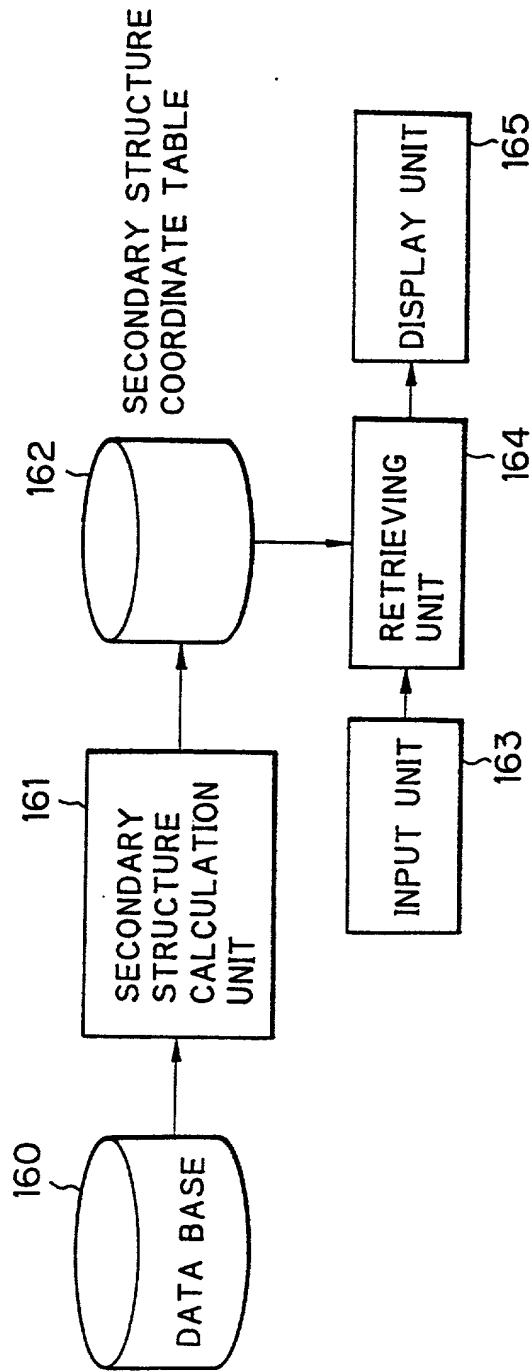


Fig. 43

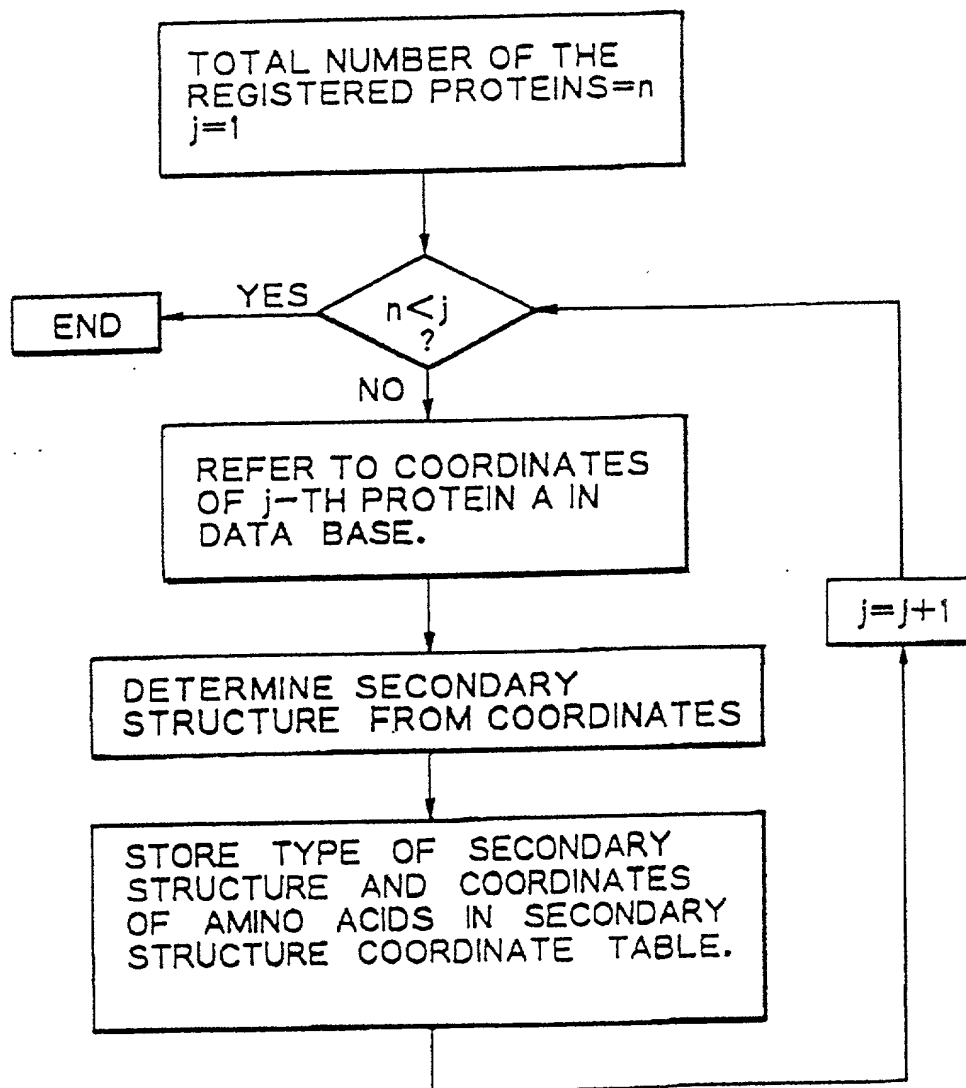


Fig. 44

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SUBSET	COORDINATES	TYPE
S1	$\{X_1, X_2, X_3, X_4, \dots X_a\}$	α - HELIX
S2	$\{X_{a+1}, X_{a+2}, \dots X_b\}$	α - HELIX
S3	$\{X_{b+1}, X_{b+2}, \dots X_c\}$	β - SHEET
S4	$\{X_{c+1}, X_{c+2}, \dots X_d\}$	β - SHEET
	\vdots	\vdots
Sn	$\{X_{l+1}, X_{l+2}, \dots X_m\}$	3 - TURN

Fig. 45

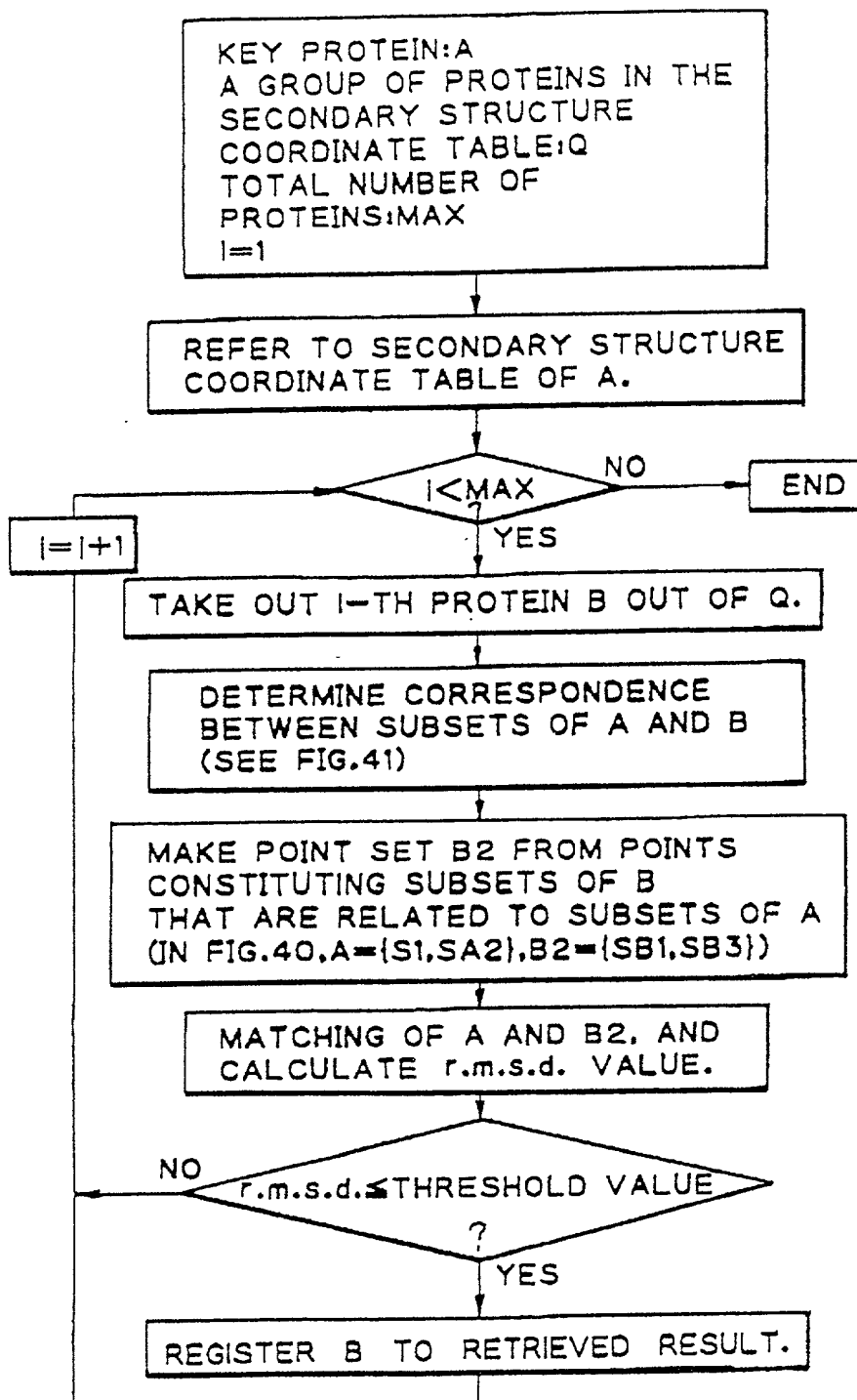
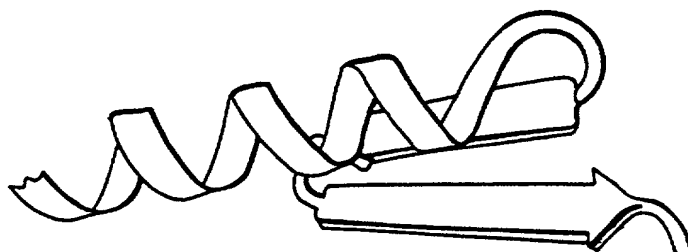
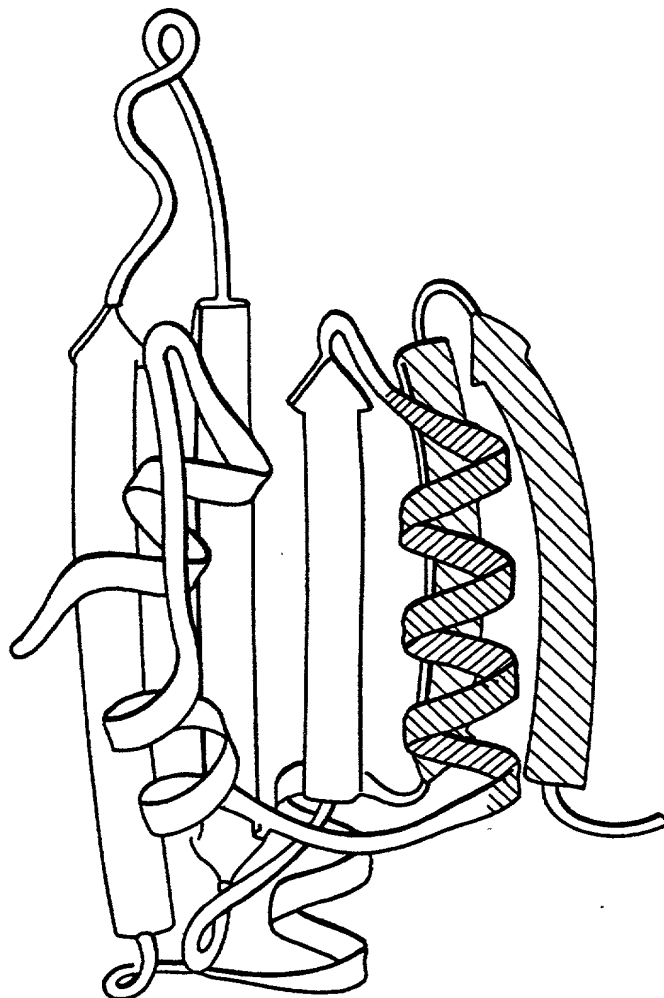


Fig. 47 A



KEY PROTEIN A

Fig. 47 B



PROTEIN B HAVING A SIMILAR STRUCTURE